


BLAST Basic Local Alignment Search Tool

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Protein Sequence (154 letters)

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|57770

Description

None

Molecule type

amino acid

Query Length

154

SEQ ID NO: 12

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jun 3, 2009 5:41 PM
Number of letters	3,072,644,098
Number of sequences	8,977,105

Entrez query none

Karlin-Altschul statistics

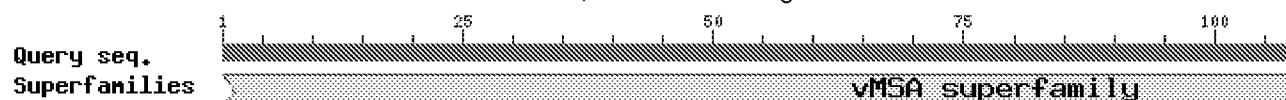
Params	Ungapped	Gapped
Lambda	0.329052	0.267
K	0.141985	0.041
H	0.532528	0.14

Results Statistics

Length adjustment	116
Effective length of query	38
Effective length of database	2031299918
Effective search space	77189396884
Effective search space used	77189396884

[Graphic Summary](#)[Show Conserved Domains](#)

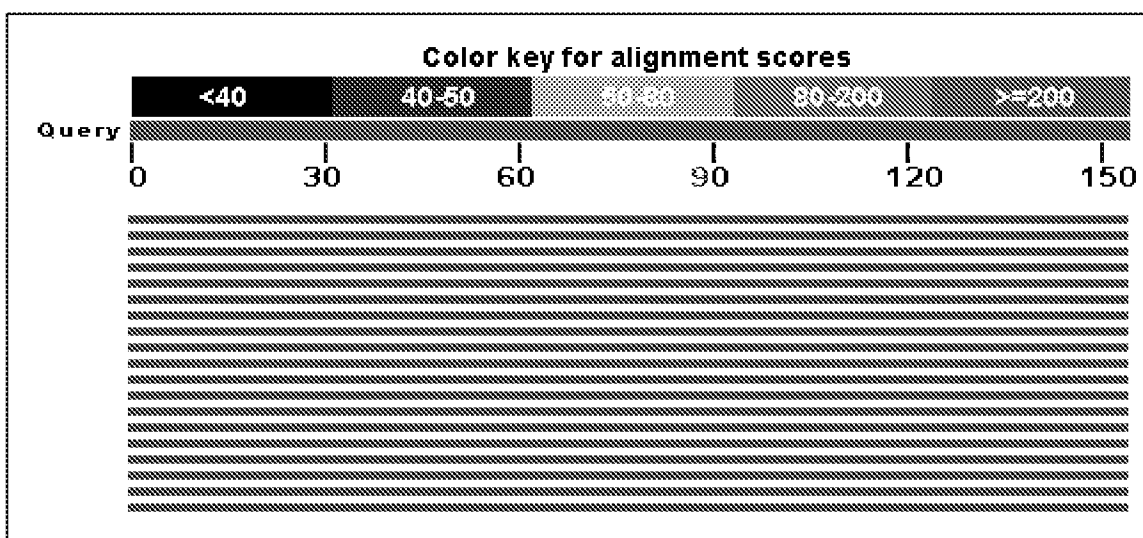
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

[\[?\]](#)

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



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Descriptions

		Score	
E			
Sequences producing significant alignments:		(Bits)	Value
gb AAD37942.1	pre-S/S protein [Hepatitis B virus]	253	3e-66
gb ABX60516.1	large S protein [Hepatitis B virus]	253	3e-66
gb AAZ23006.1	large S protein [Hepatitis B virus]	253	4e-66
gb AAC58025.2	large surface antigen [Hepatitis B virus]	253	5e-66
gb AAK97200.1 AF297624_4	large/middle/small S proteins [Hepat...	253	5e-66
gb AAZ23008.1	large S protein [Hepatitis B virus]	253	5e-66
dbj BAD91280.1	LHBs [HBV genotype A]	253	5e-66
emb CAF28873.2	preS1/preS2/S surface protein [Hepatitis B vi...	253	5e-66
gb ACW86089.1	large S protein [Hepatitis B virus]	253	5e-66
sp F03141.3 RESAG_NBVA3	RecName: Full=Large envelope protein;...	252	5e-66
dbj EAF48757.1	envelope protein [Hepatitis B virus]	252	5e-66
gb ABR04415.1	large surface protein [Hepatitis B virus]	253	5e-66
dbj BAG68757.1	PreS1-S protein [Hepatitis B virus]	253	6e-66
dbj BAD02316.1	large surface protein [Hepatitis B virus]	253	6e-66
emb CAC51294.1	large surface antigen [Hepatitis B virus]	253	6e-66
gb ACF95017.1	large S protein [Hepatitis B virus]	253	6e-66
dbj BAF81672.1	preS/S protein [Hepatitis B virus]	253	6e-66
gb AAL68820.1	surface antigen [Hepatitis B virus]	253	6e-66
gb AAR07096.1	large S protein [Hepatitis B virus]	252	6e-66
gb AAR07092.1	large S protein [Hepatitis B virus] >gb AAT904...	252	6e-66
gb ACF95172.1	large S protein [Hepatitis B virus]	252	6e-66
gb ACD65252.1	large S protein [Hepatitis B virus]	252	6e-66
gb AAK58874.1	PreS1+PreS2+HBsAg [synthetic construct] >gb AA...	252	6e-66
gb AAK07610.1	pre-S1 protein [Hepatitis B virus]	252	6e-66
gb AAR07098.1	large S protein [Hepatitis B virus]	252	6e-66
dbj BAF81676.1	preS/S protein [Hepatitis B virus]	252	6e-66
dbj BAE92978.1	large S protein [Hepatitis B virus]	252	6e-66
gb AAB47467.1	large S protein	252	6e-66
gb ACF95003.1	large S protein [Hepatitis B virus]	252	6e-66
gb ACF95193.1	large S protein [Hepatitis B virus]	252	6e-66
emb CAA84792.1	surface protein S [Hepatitis B virus]	252	6e-66
gb AAB47466.1	large S protein	252	6e-66
gb ABQ43830.1	large S protein [Hepatitis B virus]	252	6e-66
gb ACD65259.1	large S protein [Hepatitis B virus]	252	6e-66
gb AAB47468.1	large S protein	252	7e-66
gb AAD40215.1 AF090841_4	PreS1+PreS2+HBsAg [Hepatitis B virus]	252	7e-66
emb CAL29861.1	large surface antigen [Hepatitis B virus]	252	8e-66
gb AAD37946.1	pre-S/S protein [Hepatitis B virus]	252	8e-66
gb AAK97196.1 AF297623_4	large/middle/small S proteins [Hepat...	252	8e-66
gb AEQ43898.1	large S protein [Hepatitis B virus]	252	8e-66
gb AAY25271.1	large S protein [Hepatitis B virus]	252	8e-66
gb ACH81323.1	large S protein [Hepatitis B virus]	252	8e-66
gb ABQ43874.1	large S protein [Hepatitis B virus] >gb ABQ438...	252	9e-66
gb AAA45528.1	B1 wild-type molecule; ORF1 [Hepatitis B virus]	252	9e-66
emb CAQ86627.1	large S protein [Hepatitis B virus]	252	9e-66
emb CAQ86631.1	large S protein [Hepatitis B virus]	252	9e-66
gb ABQ43819.1	large S protein [Hepatitis B virus]	252	9e-66
gb ABQ43894.1	large S protein [Hepatitis B virus]	252	9e-66
gb AAY25278.1	large S protein [Hepatitis B virus]	252	9e-66
gb AAY25216.1	large S protein [Hepatitis B virus]	252	9e-66
gb AEQ43922.1	large S protein [Hepatitis B virus]	252	1e-65
gb ABW03068.1	large S protein [Hepatitis B virus]	252	1e-65
gb ABQ43823.1	large S protein [Hepatitis B virus]	252	1e-65
gb AAY25230.1	large S protein [Hepatitis B virus]	252	1e-65
gb AAP07101.1	large S protein [Hepatitis B virus]	252	1e-65
gb ABD37002.1	envelope protein [Hepatitis B virus]	252	1e-65
gb AAK97188.1 AF297621_4	large/middle/small S proteins [Hepat...	251	1e-65

gb AAV25237.1	large S protein [Hepatitis B virus]	251	1e-65
gb AEZ85698.1	large S protein [Hepatitis B virus]	251	1e-65
gb AAD37938.1	pre-S2/S protein [Hepatitis B virus]	251	1e-65
dbj BAE94219.1	Large S protein [Hepatitis B virus]	251	1e-65
gb AAQ81933.1	surface protein [Hepatitis B virus]	251	1e-65
emb CAQ86619.1	large S protein [Hepatitis B virus]	251	1e-65
gb ACN81331.1	large S protein [Hepatitis B virus]	251	1e-65
gb AAP79727.1	large S protein [Hepatitis B virus]	251	1e-65
gb AAD40219.1 AF090842.4	PreS1+PreS2+HBsAg [Hepatitis B virus]	251	1e-65
gb ABQ43931.1	large S protein [Hepatitis B virus]	251	1e-65
gb AAQ81917.1	surface protein [Hepatitis B virus]	251	1e-65
dbj EAG68764.1	PreS1-S protein [Hepatitis B virus]	251	1e-65
gb AAC58024.3	large surface antigen [Hepatitis B virus]	251	1e-65
gb ACF95018.1	middle S protein [Hepatitis B virus]	251	1e-65
gb ABQ43831.1	middle S protein [Hepatitis B virus]	251	1e-65
gb ABQ43886.1	large S protein [Hepatitis B virus]	251	2e-65
gb ABA18795.1	middle S protein [Hepatitis B virus]	251	2e-65
gb AAC58006.1	middle S protein [Hepatitis B virus] >gb AAC58...	251	2e-65
gb ABQ43899.1	middle S protein [Hepatitis B virus]	251	2e-65
gb AAM96927.1	middle S protein [Hepatitis B virus]	251	2e-65
gb ABQ43928.1	large S protein [Hepatitis B virus]	251	2e-65
gb AEQ43895.1	middle S protein [Hepatitis B virus]	251	2e-65
gb AEH04419.1	middle surface protein [Hepatitis B virus]	251	2e-65
gb ABQ43854.1	large S protein [Hepatitis B virus]	251	2e-65
dbj BAG68776.1	PreS1-S protein [Hepatitis B virus]	251	2e-65
gb ACI16298.1	S protein [Hepatitis B virus]	251	2e-65
gb ABQ43923.1	middle S protein [Hepatitis B virus] >gb ACD65...	251	2e-65
dbj BAE94223.1	Large S protein [Hepatitis B virus]	251	2e-65
gb AAT90410.1	large S protein [Hepatitis B virus]	250	2e-65
gb AAG12699.1	preS1 [Hepatitis B virus]	250	2e-65
gb ABQ43932.1	middle S protein [Hepatitis B virus]	250	2e-65
gb AAO12705.1	preS1 [Hepatitis B virus]	250	3e-65
gb ACE77880.1	middle S protein [Hepatitis B virus]	250	3e-65
gb ABI15483.1	pre-S2 protein [Hepatitis B virus] >gb ABI1549...	250	3e-65
gb ABO41307.1	S protein [Hepatitis B virus]	250	3e-65
gb ABM90718.1	HBsAg [Hepatitis B virus]	250	3e-65
gb AAO12693.1	preS1 [Hepatitis B virus]	250	3e-65
gb ABQ43887.1	middle S protein [Hepatitis B virus]	250	3e-65
gb ABL15528.1	pre-S2 protein [Hepatitis B virus]	250	3e-65
gb ABQ41295.1	S protein [Hepatitis B virus] >gb ABO41296.1 ...	250	3e-65
gb AEM90729.1	HBsAg [Hepatitis B virus]	250	3e-65
gb ABQ41267.1	S protein [Hepatitis B virus] >gb ABO41268.1 ...	250	4e-65
gb ABI15532.1	pre-S2 protein [Hepatitis B virus]	250	4e-65

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)

>gb|AAD37942.1| pre-S/S protein [Hepatitis B virus]
Length=387

Score = 253 bits (647), Expect = 3e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query	1	GGSPVCLGQNSQSPTSNNHSTSCPPICPGYRWMCLRRFIIFLFILLCLIFLLVLLDYQG	60
Sbjct	215	274
Query	61	MLPVCPLIPGSTRITSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL	120
Sbjct	275T....P.....\$.....	334
Query	121	WVWASVRFWSLSLLVPFVRWFVGLSPTVWLSAIW	154
Sbjct	335	.E.....Q.....	368

>gb|ABX60516.1| large S protein [Hepatitis B virus]
Length=383

Score = 253 bits (647), Expect = 3e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```

Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 217 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 277 .....T....P.....$..... 336
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 337 .E.....Q..... 370

```

>**gb|AAZ23006.1|** large S protein [Hepatitis B virus]
Length=398

Score = 253 bits (646), Expect = 4e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```

Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 215 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 275 .....T....P.....$..... 334
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 335 .E.....Q..... 368

```

>**gb|AAC58025.2|** large surface antigen [Hepatitis B virus]
Length=389

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```

Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 206 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 266 .....T....P.....$..... 325
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 326 .E.....Q..... 359

```

>**gb|AAK97200.1|AF297624_4** large/middle/small S proteins [Hepatitis B virus]
Length=389

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```

Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 206 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 266 .....T....P.....$..... 325
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 326 .E.....Q..... 359

```

>**gb|AAZ23008.1|** large S protein [Hepatitis B virus]
Length=398

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```

Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 215 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 275 .....T....P.....$..... 334
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 335 .E.....Q..... 368

```

>**dbj|BAD91280.1|** LHBS [HBV genotype A]
Length=400

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```
Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 217 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 277 .....T....P.....$..... 336
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 337 .E.....Q..... 370
```

>**emb|CAF28873.2|** preS1/preS2/S surface protein [Hepatitis B virus]
Length=396

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```
Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 213 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 273 .....T....P.....$..... 332
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 333 .E.....Q..... 366
```

>**gb|ACH86089.1|** large S protein [Hepatitis B virus]
Length=390

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```
Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 217 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 277 .....T....P.....$..... 336
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 337 .E.....Q..... 370
```

>**sp|P03141.3|HBSAG_HBVA3** RecName: Full=Large envelope protein; AltName: Full=Lar
protein; AltName: Full=L glycoprotein; AltName: Full=Major
surface antigen; AltName: Full=Large S protein; AltName:
Full=L-HBsAg; Short=LHB
>**emb|CAA26539.1|** unnamed protein product [Hepatitis B virus]
Length=400

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```
Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 217 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 277 .....T....P.....$..... 336
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 337 .E.....Q..... 370
```

>**dbj|BAF48757.1|** envelope protein [Hepatitis B virus]
Length=400

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```
Query 1  GGSPVCLGQNSQSPTSNSHPTSCPPICPGYRWMCLRRFIIIFLFILLCLIFLLVLLDYQG 60
Sbjct 217 .....
Query 61  MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL 120
Sbjct 277 .....T....P.....$..... 336
Query 121  VVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW 154
Sbjct 337 .E.....Q..... 370
```

>**gb|ABH04415.1|** large surface protein [Hepatitis B virus]
Length=398

Score = 253 bits (645), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query	1	GGSPVCLGQNSQSPTS	NHSPTSCPPICPGYRWMCLRRFIIIFLFILLLLCLIFLLVLLDYQG	60
Sbjct	215	274
Query	61	MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL	120	
Sbjct	275T....P.....S.....	334
Query	121	WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW	154	
Sbjct	335	.E.....Q.....	368	

>**dbj|BAG68757.1|** PreS1-S protein [Hepatitis B virus]
Length=400

Score = 253 bits (645), Expect = 6e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query	1	GGSPVCLGQNSQSPTS	NHSPTSCPPICPGYRWMCLRRFIIIFLFILLLLCLIFLLVLLDYQG	60
Sbjct	217	276
Query	61	MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL	120	
Sbjct	277T....P.....S.....	336
Query	121	WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW	154	
Sbjct	337	.E.....Q.....	370	

>**dbj|BAD02316.1|** large surface protein [Hepatitis B virus]
Length=400

Score = 253 bits (645), Expect = 6e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query	1	GGSPVCLGQNSQSPTS	NHSPTSCPPICPGYRWMCLRRFIIIFLFILLLLCLIFLLVLLDYQG	60
Sbjct	217	276
Query	61	MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL	120	
Sbjct	277T....P.....S.....	336
Query	121	WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW	154	
Sbjct	337	.E.....Q.....	370	

>**emb|CAC51294.1|** large surface antigen [Hepatitis B virus]
Length=400

Score = 253 bits (645), Expect = 6e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query	1	GGSPVCLGQNSQSPTS	NHSPTSCPPICPGYRWMCLRRFIIIFLFILLLLCLIFLLVLLDYQG	60
Sbjct	217	276
Query	61	MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL	120	
Sbjct	277T....P.....S.....	336
Query	121	WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW	154	
Sbjct	337	.E.....Q.....	370	

>**gb|ACF95017.1|** large S protein [Hepatitis B virus]
Length=400

Score = 253 bits (645), Expect = 6e-66, Method: Compositional matrix adjust.
Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query	1	GGSPVCLGQNSQSPTS	NHSPTSCPPICPGYRWMCLRRFIIIFLFILLLLCLIFLLVLLDYQG	60
Sbjct	217	276
Query	61	MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAYL	120	
Sbjct	277T....P.....S.....	336
Query	121	WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW	154	
Sbjct	337	.E.....Q.....	370	